

Study m6A Modifications Like Never Before

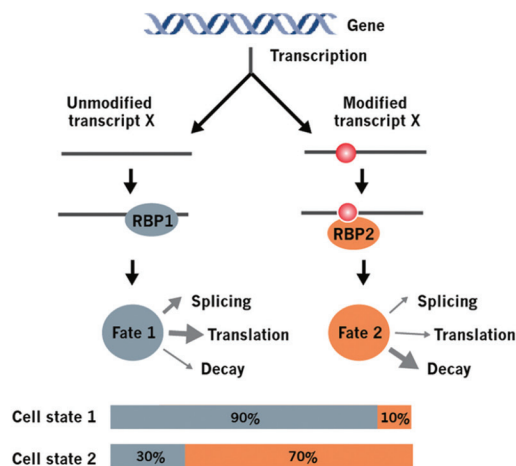


Fig. 1. m6A modified RNAs are immunoprecipitated and compared with the input RNAs in two-color channels of the Epitranscriptomic Array to accurately measure the modification percentage and abundance level for each transcript. The percentage of modification of “transcript a” RNA determines its different cell fates, e.g. for protein translation or RNA decay.

Epitranscriptomic Array

- Quantifying the percentage of modification for each transcript
- Coverage of mRNAs, lncRNAs, circRNAs and more
- RNA modifications at transcript-specific level
- Low sample amount, starting from 1 ug total RNA

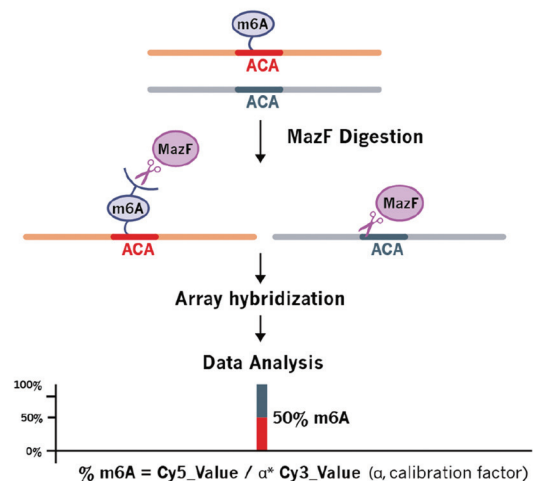


Fig. 2. Unmethylated (ACA) sites, but not methylated (m6ACA) sites, are cleaved by RNase MazF. The MazF treated and corresponding untreated sites are compared in two-color channels of the m6A Single Nucleotide Array to accurately quantify the m6A modification percentage, and abundance level at precise single nucleotide resolution.

m6A Single Nucleotide Array

- A new orthogonal methodology for m6A detection
- Single-Nucleotide resolution for m6A site location
- Quantifying the percentage of m6A site modification
- Reliable m6A site collection and systematic annotations
- Low sample amount, starting from 1 ug total RNA

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CE-IVD, Annex III
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EN 14476:2017



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Horsington, J., et al. "Inactivation of foot-and-mouth disease virus...for safe transport and processing in low-containment labs" *Journal of virological methods*. **2020**
Bundgaard-Nielsen, C., et al. "Interpersonal variations in gut microbiota profiles supersedes the effects of differing fecal storage conditions." *Nature*. **2018**
Lalitha, P., et al. "Unbiased pathogen detection and host gene profiling for conjunctivitis." *Ophthalmology*. **2019**
Nowotny N, Kolodziejek J. Middle East respiratory syndrome coronavirus (MERS-CoV) in dromedary camels, Oman, 2013. *Euro Surveill*. **2014**
Galanti, M, Birger, R, Ud-Dean, M, et al. Longitudinal active sampling for respiratory viral infections across age groups. *Influenza Other Respi Viruses*. **2019**

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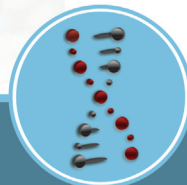
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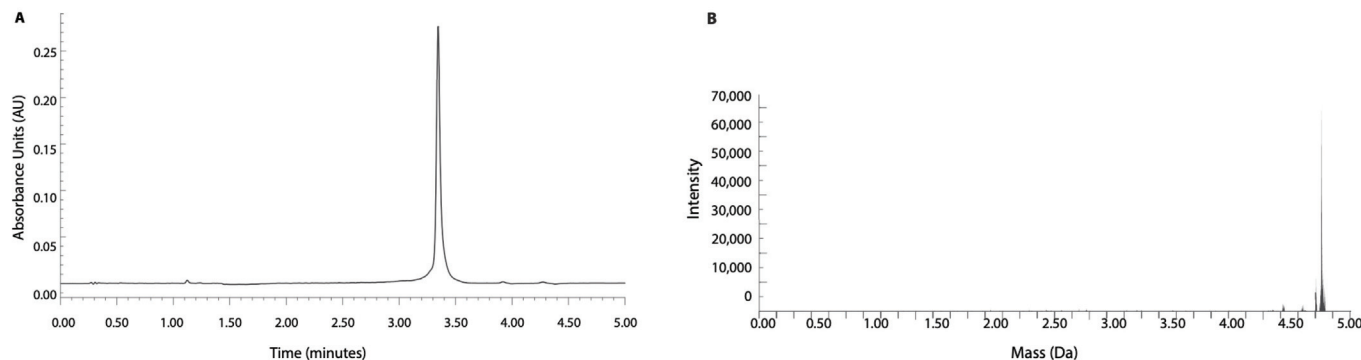
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(A) UPLC analysis showing >90% pure full-length material. (B) Mass spec analysis illustrating the correct mass.

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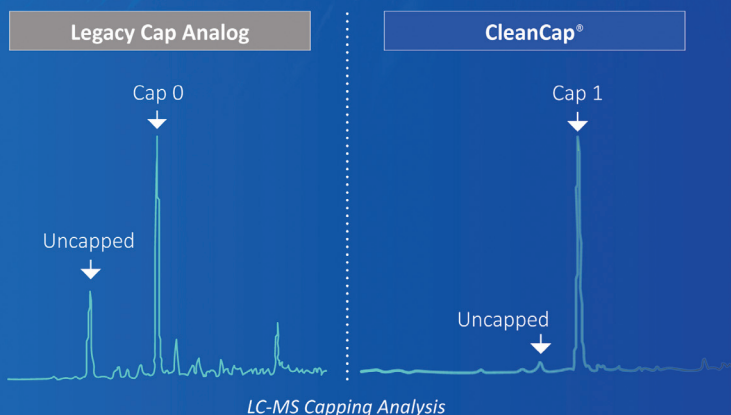
in Co-Transcriptional mRNA Capping

CleanCap® demonstrates superior performance versus legacy co-transcriptional capping methods

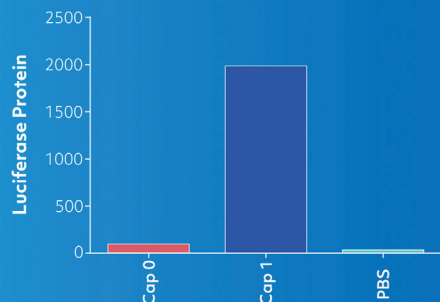
	Legacy Cap Analogs		CleanCap®	
Natural Cap	No	⊖	Yes	⊕
Immunogenic	Yes	⊖	Reduced Immunogenicity	⊕
Capping Efficiency	~70%	⊖	~95%	⊕
Yield/mL Transcription	1.5 mg/mL	⊖	4 mg/mL	⊕
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Available Therapeutic Licenses	No	⊖	Yes	⊕

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Luciferase mRNA was formulated with Lunar Lipids and injected by tail vein into mice. At 6 hours, luciferase was measured by western blot in mouse liver. Data courtesy of Arcturus Therapeutics.

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